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RAW SEQUENCE LISTING   DATE: 08/15/2001
PATENT APPLICATION: **US/09/530,233**   TIME: 08:21:43

Input Set : **A:\Mcgill.app**
Output Set: **N:\CRF3\08132001\I530233.raw**

```
 3 <110> APPLICANT: Seguela, Philippe
 4        Babinski, Kazimierz
 5        McGill University
 7 <120> TITLE OF INVENTION: DNA ENCODING A HUMAN PROTON-GATED ION CHANNEL AND USES
 8        THEREOF
10 <130> FILE REFERENCE: 641050.90021
12 <140> CURRENT APPLICATION NUMBER: US/09/530,233
13 <141> CURRENT FILING DATE: 1997-10-29
15 <150> PRIOR APPLICATION NUMBER: US09/530,233
16 <151> PRIOR FILING DATE: 1997-10-29
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1732
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (22)..(1614)
31 <400> SEQUENCE: 1
32 tcgcacgacg cggttctggc c atg aag ccc acc tca ggc cca gag gag gcc     51
33                         Met Lys Pro Thr Ser Gly Pro Glu Glu Ala
34                          1               5                  10
36 cgg cgg cag ccc tcg gac atc cgc gtg ttc gcc agc aac tgc tcg atg     99
37 Arg Arg Gln Pro Ser Asp Ile Arg Val Phe Ala Ser Asn Cys Ser Met
38              15                  20                  25
40 cac ggg ctg ggc cac gtc ttc ggg cca ggc agc ctg agc ctg cgc cgg    147
41 His Gly Leu Gly His Val Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg
42              30                  35                  40
44 ggg atg tgg gca gcg gcc gtg gtc ctg tca gtg gcc acc ttc ctc tac    195
45 Gly Met Trp Ala Ala Ala Val Val Leu Ser Val Ala Thr Phe Leu Tyr
46              45                  50                  55
48 cag gtg gct gag agg gtg cgc tac tac agg gag ttc cac cac cag act    243
49 Gln Val Ala Glu Arg Val Arg Tyr Tyr Arg Glu Phe His His Gln Thr
50          60                  65                  70
52 gcc ctg gat gag cga gaa agc cac cgg ctc gtc ttc ccg gct gtc acc    291
53 Ala Leu Asp Glu Arg Glu Ser His Arg Leu Val Phe Pro Ala Val Thr
54   75                  80                  85                  90
56 ctg tgc aac atc aac cca ctg cgc cgc tcg cgc cta acg ccc aac gac    339
57 Leu Cys Asn Ile Asn Pro Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp
58              95                 100                 105
60 ctg cac tgg gct ggg tct gcg ctg ctg ggc ctg gat ccc gca gag cac    387
61 Leu His Trp Ala Gly Ser Ala Leu Leu Gly Leu Asp Pro Ala Glu His
62             110                 115                 120
64 gcc gcc ttc ctg cgc gcc ctg ggc cgg ccc cct gca ccg ccc ggc ttc    435
65 Ala Ala Phe Leu Arg Ala Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe
66             125                 130                 135
```

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```
68 atg ccc agt ccc acc ttt gac atg gcg caa ctc tat gcc cgt gct ggg   483
69 Met Pro Ser Pro Thr Phe Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly
70     140                 145                 150
72 cac tcc ctg gat gac atg ctg ctg gac tgt cgc ttc cgt ggc caa cct   531
73 His Ser Leu Asp Asp Met Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro
74 155                 160                 165                 170
76 tgt ggg cct gag aac ttc acc acg atc ttc acc cgg atg gga aag tgc   579
77 Cys Gly Pro Glu Asn Phe Thr Thr Ile Phe Thr Arg Met Gly Lys Cys
78                 175                 180                 185
80 tac aca ttt aac tct ggc gct gat ggg gca gag ctg ctc acc act act   627
81 Tyr Thr Phe Asn Ser Gly Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr
82                 190                 195                 200
84 agg ggt ggc atg ggc aat ggg ctg gac atc atg ctg gac gtg cag cag   675
85 Arg Gly Gly Met Gly Asn Gly Leu Asp Ile Met Leu Asp Val Gln Gln
86         205                 210                 215
88 gag gaa tat cta cct gtg tgg agg gac aat gag gag acc ccg ttt gag   723
89 Glu Glu Tyr Leu Pro Val Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu
90     220                 225                 230
92 gtg ggg atc cga gtg cag atc cac agc cag gag gag ccg ccc atc atc   771
93 Val Gly Ile Arg Val Gln Ile His Ser Gln Glu Glu Pro Pro Ile Ile
94 235                 240                 245                 250
96 gat cag ctg ggc ttg ggg gtg tcc ccg ggc tac cag acc ttt gtt tct   819
97 Asp Gln Leu Gly Leu Gly Val Ser Pro Gly Tyr Gln Thr Phe Val Ser
98                 255                 260                 265
100 tgc cag cag cag cag ctg agc ttc ctg cca ccg ccc tgg ggc gat tgc   867
101 Cys Gln Gln Gln Gln Leu Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys
102                 270                 275                 280
104 agt tca gca tct ctg aac ccc aac tat gag cca gag ccc tct gat ccc   915
105 Ser Ser Ala Ser Leu Asn Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro
106         285                 290                 295
108 cta ggc tcc ccc agc ccc agc ccc agc cct ccc tat acc ctt atg ggg   963
109 Leu Gly Ser Pro Ser Pro Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly
110     300                 305                 310
112 tgt cgc ctg gcc tgc gaa acc cgc tac gtg gct cgg aag tgc ggc tgc   1011
113 Cys Arg Leu Ala Cys Glu Thr Arg Tyr Val Ala Arg Lys Cys Gly Cys
114 315                 320                 325                 330
116 cga atg gtg tac atg cca ggc gac gtg cca gtg tgc agc ccc cag cag   1059
117 Arg Met Val Tyr Met Pro Gly Asp Val Pro Val Cys Ser Pro Gln Gln
118                 335                 340                 345
120 tac aag aac tgt gcc cac ccg gcc ata gat gcc atc ctt cgc aag gac   1107
121 Tyr Lys Asn Cys Ala His Pro Ala Ile Asp Ala Ile Leu Arg Lys Asp
122                 350                 355                 360
124 tcg tgc gcc tgc ccc aac ccg tgc gcc agc acg cgc tac gcc aag gag   1155
125 Ser Cys Ala Cys Pro Asn Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu
126         365                 370                 375
128 ctc tcc atg gtg cgg atc ccg agc cgc gcc gcc gcg cgc ttc ctg gcc   1203
129 Leu Ser Met Val Arg Ile Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala
130     380                 385                 390
132 cgg aag ctc aac cgc agc gag gcc tac atc gcg gag aac gtg ctg gcc   1251
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```
133 Arg Lys Leu Asn Arg Ser Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala
134 395             400             405             410
136 ctg gac atc ttc ttt gag gcc ctc aac tat gag acc gtg gag cag aag   1299
137 Leu Asp Ile Phe Phe Glu Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys
138             415             420             425
140 aag gcc tat gag atg tca gag ctg ctt ggt gac att ggg ggc cag atg   1347
141 Lys Ala Tyr Glu Met Ser Glu Leu Leu Gly Asp Ile Gly Gly Gln Met
142             430             435             440
144 ggc ctt ttc atc ggg gcc agc ctg ctc acc atc ctc gag atc cta gac   1395
145 Gly Leu Phe Ile Gly Ala Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp
146             445             450             455
148 tac ctc tgt gag gtg ttc cga gac aag gtc ctg gga tat ttc tgg aac   1443
149 Tyr Leu Cys Glu Val Phe Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn
150     460             465             470
152 cga cag cac tcc caa agg cac tcc agc acc aat ctg ctt cag gaa ggg   1491
153 Arg Gln His Ser Gln Arg His Ser Ser Thr Asn Leu Leu Gln Glu Gly
154 475             480             485             490
156 ctg ggc agc cat cga acc caa gtt ccc cac ctc agc ctg ggc ccc aga   1539
157 Leu Gly Ser His Arg Thr Gln Val Pro His Leu Ser Leu Gly Pro Arg
158             495             500             505
160 cct ccc acc cct ccc tgt gcc gtc acc aag act ctc tcc gcc tcc cac   1587
161 Pro Pro Thr Pro Pro Cys Ala Val Thr Lys Thr Leu Ser Ala Ser His
162             510             515             520
164 cgc acc tgc tac ctt gtc aca cag ctc tagacctgct gtctgtgtcc         1634
165 Arg Thr Cys Tyr Leu Val Thr Gln Leu
166         525             530
168 tcggagcccc gccctgacat cctggacatg cctagcctgc acgtagcttt tccgtcttca 1694
170 ccccaaataa agtcctaatg catcaaaaaa aaaaaaaa                          1732
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173 <210> SEQ ID NO: 2
174 <211> LENGTH: 531
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 2

```
179 Met Lys Pro Thr Ser Gly Pro Glu Glu Ala Arg Arg Gln Pro Ser Asp
180  1               5               10              15
182 Ile Arg Val Phe Ala Ser Asn Cys Ser Met His Gly Leu Gly His Val
183             20              25              30
185 Phe Gly Pro Gly Ser Leu Ser Leu Arg Arg Gly Met Trp Ala Ala Ala
186             35              40              45
188 Val Val Leu Ser Val Ala Thr Phe Leu Tyr Gln Val Ala Glu Arg Val
189     50              55              60
191 Arg Tyr Tyr Arg Glu Phe His His Gln Thr Ala Leu Asp Glu Arg Glu
192 65              70              75              80
194 Ser His Arg Leu Val Phe Pro Ala Val Thr Leu Cys Asn Ile Asn Pro
195             85              90              95
197 Leu Arg Arg Ser Arg Leu Thr Pro Asn Asp Leu His Trp Ala Gly Ser
198             100             105             110
200 Ala Leu Leu Gly Leu Asp Pro Ala Glu His Ala Ala Phe Leu Arg Ala
201             115             120             125
```

```
203 Leu Gly Arg Pro Pro Ala Pro Pro Gly Phe Met Pro Ser Pro Thr Phe
204     130             135         140
206 Asp Met Ala Gln Leu Tyr Ala Arg Ala Gly His Ser Leu Asp Asp Met
207 145             150             155             160
209 Leu Leu Asp Cys Arg Phe Arg Gly Gln Pro Cys Gly Pro·Glu Asn Phe
210             165             170             175
212 Thr Thr Ile Phe Thr Arg Met Gly Lys Cys Tyr Thr Phe Asn Ser Gly
213         180             185             190
215 Ala Asp Gly Ala Glu Leu Leu Thr Thr Thr Arg Gly Gly Met Gly Asn
216         195             200             205
218 Gly Leu Asp Ile Met Leu Asp Val Gln Gln Glu Glu Tyr Leu Pro Val
219     210             215             220
221 Trp Arg Asp Asn Glu Glu Thr Pro Phe Glu Val Gly Ile Arg Val Gln
222 225             230             235             240
224 Ile His Ser Gln Glu Glu Pro Pro Ile Ile Asp Gln Leu Gly Leu Gly
225             245             250             255
227 Val Ser Pro Gly Tyr Gln Thr Phe Val Ser Cys Gln Gln Gln Gln Leu
228             260             265             270
230 Ser Phe Leu Pro Pro Pro Trp Gly Asp Cys Ser Ser Ala Ser Leu Asn
231         275             280             285
233 Pro Asn Tyr Glu Pro Glu Pro Ser Asp Pro Leu Gly Ser Pro Ser Pro
234     290             295             300
236 Ser Pro Ser Pro Pro Tyr Thr Leu Met Gly Cys Arg Leu Ala Cys Glu
237 305             310             315             320
239 Thr Arg· Tyr Val Ala Arg Lys Cys Gly Cys Arg Met Val Tyr Met Pro
240             325             330             335
242 Gly Asp Val Pro Val Cys Ser Pro Gln Gln Tyr Lys Asn Cys Ala His
243             340             345             350
245 Pro Ala Ile Asp Ala Ile Leu Arg Lys Asp Ser Cys Ala Cys Pro Asn
246         355             360             365
248 Pro Cys Ala Ser Thr Arg Tyr Ala Lys Glu Leu Ser Met Val Arg Ile
249     370             375             380
251 Pro Ser Arg Ala Ala Ala Arg Phe Leu Ala Arg Lys Leu Asn Arg Ser
252 385             390             395             400
254 Glu Ala Tyr Ile Ala Glu Asn Val Leu Ala Leu Asp Ile Phe Phe Glu
255             405             410             415
257 Ala Leu Asn Tyr Glu Thr Val Glu Gln Lys Lys Ala Tyr Glu Met Ser
258             420             425             430
260 Glu Leu Leu Gly Asp Ile Gly Gly Gln Met Gly Leu Phe Ile Gly Ala
261         435             440             445
263 Ser Leu Leu Thr Ile Leu Glu Ile Leu Asp Tyr Leu Cys Glu Val Phe
264     450             455             460
266 Arg Asp Lys Val Leu Gly Tyr Phe Trp Asn Arg Gln His Ser Gln Arg
267 465             470             475             480
269 His Ser Ser Thr Asn Leu Leu Gln Glu Gly Leu Gly Ser His Arg Thr
270             485             490             495
272 Gln Val Pro His Leu Ser Leu Gly Pro Arg Pro Pro Thr Pro Pro Cys
273         500             505             510
275 Ala Val Thr Lys Thr Leu Ser Ala Ser His Arg Thr Cys Tyr Leu Val
```

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Input Set : **A:\Mcgill.app**
Output Set: **N:\CRF3\08132001\I530233.raw**

```
276          515              520              525
278 Thr Gln Leu
279      530
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 17
284 <212> TYPE: PRT
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <221> NAME/KEY: PEPTIDE
289 <222> LOCATION: (2)
290 <223> OTHER INFORMATION: "Xaa = unidentified amino acid."
292 <220> FEATURE:
293 <221> NAME/KEY: PEPTIDE
294 <222> LOCATION: (11)
295 <223> OTHER INFORMATION: "Xaa = unidentified amino acid."
297 <220> FEATURE:
298 <221> NAME/KEY: PEPTIDE
299 <222> LOCATION: (13)..(14)
300 <223> OTHER INFORMATION: "Xaa = unidentified amino acid."
302 <220> FEATURE:
303 <221> NAME/KEY: PEPTIDE
304 <222> LOCATION: (16)
305 <223> OTHER INFORMATION: Xaa = unidentified amino acid."
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Protein Motif
310 <400> SEQUENCE: 3
```
W--> **311 Leu Xaa Phe Pro Ala Val Thr Leu Cys Asn Xaa Asn Xaa Xaa Arg Xaa**
```
312   1             5               10             15
314 Ser
318 <210> SEQ ID NO: 4
319 <211> LENGTH: 20
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence:
325       Oligonucleotide Primer
327 <400> SEQUENCE: 4
328 tcagtggcca ccttcctcta                                        20
331 <210> SEQ ID NO: 5
332 <211> LENGTH: 21
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence:
338       Oligonucleotide Primer
340 <400> SEQUENCE: 5
341 acagtccagc agcatgtcat c                                      21
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VERIFICATION SUMMARY   DATE: 08/15/2001
PATENT APPLICATION: **US/09/530,233**   TIME: 08:21:44

Input Set : **A:\Mcgill.app**
Output Set: **N:\CRF3\08132001\I530233.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3